

#8

SEQUENCE LISTING

<110> Huse, William D.
Wu, Herren



<120> Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
Acids Encoding Same and Methods of Use

<130> P-IX 3536

<140> US 09/339,922

<141> 1999-06-24

<160> 112

<170> PatentIn Ver. 2.1

<210> 1

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(351)

<220>

<223> Description of Artificial Sequence: grafted
antibody variable region

<400> 1

cag gtg cag ctg gtg gag tct ggc gga ggc gtt gtg cag cct gga agg 48
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

gac atg tct tgg gtt cgc cag gct ccg ggc aag ggt ctg gag tgg gtc 144
Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca aaa gtt agt agt ggt ggt ggt agc acc tac tat tta gac act gtg 192
Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
50 55 60

cag ggc cga ttc acc atc tcc aga gac aat agt aag aac acc cta tac 240

Gln	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70					75				80		
ctg	caa	atg	aac	tct	ctg	aga	gcc	gag	gac	aca	gcc	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
gca	aga	cat	aac	tac	ggc	agt	ttt	gct	tac	tgg	ggc	caa	ggg	act	aca	336
Ala	Arg	His	Asn	Tyr	Gly	Ser	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	
			100					105					110			
gtg	act	gtt	tct	agt												351
Val	Thr	Val	Ser	Ser												
			115													

<210> 2
 <211> 117
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: grafted
 antibody variable region

<400> 2																
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	
			20					25					30			
Asp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Ala	Lys	Val	Ser	Ser	Gly	Gly	Gly	Ser	Thr	Tyr	Tyr	Leu	Asp	Thr	Val	
	50					55					60					
Gln	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70					75				80		
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
Ala	Arg	His	Asn	Tyr	Gly	Ser	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	
			100					105					110			
Val	Thr	Val	Ser	Ser												
			115													

<210> 3
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(321)

<220>
 <223> Description of Artificial Sequence: grafted
 antibody variable region

<400> 3
 gag att gtg cta act cag tct cca gcc acc ctg tct ctc agc cca gga 48
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 gaa agg gcg act ctt tcc tgc cag gcc agc caa agt att agc aac cac 96
 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
 20 25 30
 cta cac tgg tat caa caa agg cct ggt caa gcc cca agg ctt ctc atc 144
 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 aag tat cgt tcc cag tcc atc tct ggg atc ccc gcc agg ttc agt ggc 192
 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 agt gga tca ggg aca gat ttc acc ctc act atc tcc agt ctg gag cct 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80
 gaa gat ttt gca gtc tat tac tgt caa cag agt ggc agc tgg cct cac 288
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
 85 90 95
 acg ttc gga ggg ggg acc aag gtg gaa att aag 321
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 4
 <211> 107
 <212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: grafted
antibody variable region

<400> 4

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
20 25 30

Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 5

<211> 351

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(351)

<400> 5

gaa gtg cag ctg gtg gag tct ggg gga ggc tta gtg aag cct gga agg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc gct ttc agt agc tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
20 25 30

gac atg tct tgg gtt cgc cag att ccg gag aag agg ctg gag tgg gtc 144
Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val

35	40	45	
gca aaa gtt agt agt ggt ggt ggt agc acc tac tat tta gac act gtg			192
Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val			
50	55	60	
cag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc cta tac			240
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr			
65	70	75	80
ctg caa atg agc agt ctg aac tct gag gac aca gcc atg tat tac tgt			288
Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys			
85	90	95	
gca aga cat aac tac ggc agt ttt gct tac tgg ggc caa ggg act ctg			336
Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu			
100	105	110	
gtc act gtc tct gca			351
Val Thr Val Ser Ala			
115			
<210> 6			
<211> 117			
<212> PRT			
<213> Mus musculus			
<400> 6			
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg			
1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr			
20	25	30	
Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val			
35	40	45	
Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val			
50	55	60	
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys			
85	90	95	
Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu			

100

105

110

Val Thr Val Ser Ala
115

<210> 7

<211> 321

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(321)

<400> 7

gat	att	gtg	cta	act	cag	tct	cca	gcc	acc	ctg	tct	gtg	aca	cca	gga	48
Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Thr	Pro	Gly	
1				5					10					15		

gat	agc	gtc	agt	ctt	tcc	tgc	cag	gcc	agc	caa	agt	att	agc	aac	cac	96
Asp	Ser	Val	Ser	Leu	Ser	Cys	Gln	Ala	Ser	Gln	Ser	Ile	Ser	Asn	His	
			20					25					30			

cta	cac	tgg	tat	caa	caa	aaa	tca	cat	gag	tct	cca	agg	ctt	ctc	atc	144
Leu	His	Trp	Tyr	Gln	Gln	Lys	Ser	His	Glu	Ser	Pro	Arg	Leu	Leu	Ile	
		35					40					45				

aag	tat	cgt	tcc	cag	tcc	atc	tct	ggg	atc	ccc	tcc	agg	ttc	agt	ggc	192
Lys	Tyr	Arg	Ser	Gln	Ser	Ile	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						

agt	gga	tca	ggg	aca	gat	ttc	gct	ctc	agt	atc	aac	agt	gtg	gag	act	240
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ala	Leu	Ser	Ile	Asn	Ser	Val	Glu	Thr	
	65				70				75				80			

gaa	gat	ttt	gga	atg	tat	ttc	tgt	caa	cag	agt	ggc	agc	tgg	cct	cac	288
Glu	Asp	Phe	Gly	Met	Tyr	Phe	Cys	Gln	Gln	Ser	Gly	Ser	Trp	Pro	His	
			85					90					95			

acg	ttc	gga	ggg	ggg	acc	aag	ctg	gaa	att	aag						321
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
		100					105									

<210> 8

<211> 107

<212> PRT

<213> Mus musculus

<400> 8

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
65 70 75 80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 9

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 9

cagggtgcagc tgggtggagtc tggggggaggc gttgtgcagc ctggaaggtc cctgagactc 60
tcctgtgcag cctctggatt cacc 84

<210> 10

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

oligonucleotide

<400> 10

aacttttgcg acccactcca gacccttgcc cggagcctgg cgaacccaag acatgtcata 60
gctactgaag gtgaatccag aggc 84

<210> 11

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 11

tgggtcgcaa aagttagtag tgggtggtggt agcacctact atttagacac tgtgcagggc 60
cgattcacca tctccagaga caatagt 87

<210> 12

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 12

tgcacagtaa tacacggctg tgtcctcggc tctcagagag ttcatttgca ggtatagggt 60
gttcttacta ttgtctctgg a 81

<210> 13

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 13

gtgtattact gtgcaagaca taactacggc agttttgctt actggggcca agggactaca 60
gtgactgttt ctagt 75

<210> 14
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 14
gagattgtgc taactcagtc tccagccacc ctgtctctca gcccaggaga aagggcgact 60
ctttcctgcc aggccagcca aagtatt 87

<210> 15
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 15
gatgagaagc cttggggctt gaccaggcct ttgttgatac cagtgtagggt ggttgctaata 60
actttggctg gc 72

<210> 16
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 16
ccaaggcttc tcacwasta tcgttcccag tccatctctg ggatccccgc caggttcagt 60
ggcagtgat caggacaga ttcc 84

<210> 17
<211> 81
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 17

gctgccactc tgttgacagw aatagactgc aaaatcttca ggctccagac tggagatagt 60
gagggtgaaa tctgtccctg a 81

<210> 18

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 18

caacagagtgc gcagctggcc tcacacgttc ggagggggga ccaaggtgga aattaag 57

<210> 19

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 19

gcccaaccag ccatggccga tattgtgcta actcag 36

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 20

acagttggtg cagcatcagc 20

<210> 21
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 21
acccctgtgg caaaagccga agtgcagctg gtggag 36

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 22
gatgggggtg tcgttttggc 20

<210> 23
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 23
gagattgtgc taactcagtc tccagccacc ctgtctctca gcccaggaga aagggcgact 60
ctttcctgcc aggccagcca aagtatt 87

<210> 24
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 24
ttagatgaga agccttgagg ctgaccagg cctttgttga taccagtga ggtggttgct 60
aatactttgg ctggc 75

<210> 25
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 25
ccaaggcttc tcactaata tegtccag tccatctctg ggatccccgc caggttcagt 60
ggcagtgat caggacaga ttcc 84

<210> 26
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 26
gctgccactc tgtgacagt aatagactgc aaaatcttca ggctccagac tggagatagt 60
gagggtgaaa tctgtcctg a 81

<210> 27
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 27
caacagagtg gcagctggcc tcacacgttc ggagggggga ccaaggtgga aattaag 57

<210> 28

<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: antigen

<400> 28

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1 5 10

<210> 29

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 29

gctactgaag gcgaatccag ag

22

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (11)..(13)

<223> NNN = codon specifying any amino acid other than
Lys.

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 30

gggaacgata nnngatgaga agc

23

<210> 31

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: grafted
antibody variable region

<220>

<221> variation

<222> (145)..(147)

<223> NNN=CGT OR ATG;

<400> 31

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gagattgtgc taactcagtc tccagccacc ctgtctctca gcccaggaga aagggcgact 60
ctttcctgcc aggccagcca aagtattagc aaccacctac actggtatca acaaaggcct 120
gggtcaagccc caaggcttct catcnntat cgttccagc ccatctctgg gatccccgcc 180
aggttcagtg gcagtggatc agggacagat ttcaccctca ctatctccag tctggagcct 240
gaagattttg cagtctatta ctgtcaacag agtggcagct ggcctcacac gttcggaggg 300
gggaccaagg tggaaattaa g                                     321
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<210> 32

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (49)

<223> Xaa = Arg or Met

<220>

<223> Description of Artificial Sequence: grafted
antibody variable region

<400> 32

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
  1             5             10             15
```

```
Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
      20             25             30
```

```
Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
      35             40             45
```

```
Xaa Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
      50             55             60
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
      65             70             75             80
```

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 33
<211> 30
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(30)

<400> 33
gga ttc acc ttc agt agc tat gac atg tct 30
Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser
1 5 10

<210> 34
<211> 10
<212> PRT
<213> Mus musculus

<400> 34
Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser
1 5 10

<210> 35
<211> 30
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(30)

<400> 35
tgg gtc gca aaa gtt agt agt ggt ggt ggt 30
Trp Val Ala Lys Val Ser Ser Gly Gly Gly
1 5 10

<210> 36
<211> 10
<212> PRT
<213> Mus musculus

<400> 36
Trp Val Ala Lys Val Ser Ser Gly Gly Gly
1 5 10

<210> 37
<211> 30
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(30)

<400> 37
agc acc tac tat tta gac act gtg cag ggc
Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly
1 5 10

30

<210> 38
<211> 10
<212> PRT
<213> Mus musculus

<400> 38
Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly
1 5 10

<210> 39
<211> 30
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(30)

<400> 39

gca aga cat aac tac ggc agt ttt gct tac
Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr
1 5 10

30

<210> 40
<211> 10
<212> PRT
<213> Mus musculus

<400> 40
Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr
1 5 10

<210> 41
<211> 39
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(39)

<400> 41
cag gcc agc caa agt att agc aac cac cta cac tgg tat
Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr
1 5 10

39

<210> 42
<211> 13
<212> PRT
<213> Mus musculus

<400> 42
Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr
1 5 10

<210> 43
<211> 33
<212> DNA
<213> Mus musculus

<220>

<221> CDS
<222> (1)..(33)

<400> 43
ctt ctc atc cgt tat cgt tcc cag tcc atc tct
Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser
1 5 10

33

<210> 44
<211> 11
<212> PRT
<213> Mus musculus

<400> 44
Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser
1 5 10

<210> 45
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 45
caa cag agt ggc agc tgg cct cac acg
Gln Gln Ser Gly Ser Trp Pro His Thr
1 5

27

<210> 46
<211> 9
<212> PRT
<213> Mus musculus

<400> 46
Gln Gln Ser Gly Ser Trp Pro His Thr
1 5

<210> 47
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 47
gga act acc ttc agt agc tat gac atg tct 30
Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser
1 5 10

<210> 48
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 48
Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser
1 5 10

<210> 49
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 49
gga ttc acc tgg agt agc tat gac atg tct 30
Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser
1 5 10

<210> 50
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 50
Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser
1 5 10

<210> 51
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 51
gga ttc acc ttc ctg agc tat gac atg tct 30
Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser
1 5 10

<210> 52
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 52
Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser
1 5 10

<210> 53
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 53
tgg gtc gca aaa gtt aaa agt ggt ggt ggt 30
Trp Val Ala Lys Val Lys Ser Gly Gly Gly
1 5 10

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 54
Trp Val Ala Lys Val Lys Ser Gly Gly Gly
1 5 10

<210> 55
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 55
agc acc tac tat cct gac act gtg cag ggc 30
Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly
1 5 10

<210> 56
 <211> 10
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 56
 Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly
 1 5 10

<210> 57
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(30)

<220>
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 57
 agc acc tac tat tta gac act gtg gag ggc 30
 Ser Thr Tyr Tyr Leu Asp Thr Val Glu Gly
 1 5 10

<210> 58
 <211> 10
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 58
 Ser Thr Tyr Tyr Leu Asp Thr Val Glu Gly
 1 5 10

<210> 59
 <211> 30

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 59
gca aga cat aac cat ggc agt ttt gct tac
Ala Arg His Asn His Gly Ser Phe Ala Tyr
1 5 10

30

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 60
Ala Arg His Asn His Gly Ser Phe Ala Tyr
1 5 10

<210> 61
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 61
gca aga cat aac tac ggc agt tat gct tac
Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr
1 5 10

30

<210> 62
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 62
Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr
1 5 10

<210> 63
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 63
gca aga cat aac tac ggc agt ttt gat tac 30
Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr
1 5 10

<210> 64
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 64
Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr
1 5 10

<210> 65
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 65
gca aga cat aac tac ggc agt ttt tat tac
Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr
1 5 10

30

<210> 66
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 66
Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr
1 5 10

<210> 67
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 67
gca aga cat aac tac ggc agt ttt gct tct
Ala Arg His Asn Tyr Gly Ser Phe Ala Ser
1 5 10

30

<210> 68
 <211> 10
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 68
 Ala Arg His Asn Tyr Gly Ser Phe Ala Ser
 1 5 10

<210> 69
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(30)

<220>
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 69
 gca aga cat aac tac ggc agt ttt gct act 30
 Ala Arg His Asn Tyr Gly Ser Phe Ala Thr
 1 5 10

<210> 70
 <211> 10
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 70
 Ala Arg His Asn Tyr Gly Ser Phe Ala Thr
 1 5 10

<210> 71
 <211> 30

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 71
gca aga cat aac tac ggc agt ttt gct gat
Ala Arg His Asn Tyr Gly Ser Phe Ala Asp
1 5 10

30

<210> 72
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 72
Ala Arg His Asn Tyr Gly Ser Phe Ala Asp
1 5 10

<210> 73
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 73
gca aga cat aac tac ggc agt ttt gct gag
Ala Arg His Asn Tyr Gly Ser Phe Ala Glu
1 5 10

30

<210> 74
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 74
Ala Arg His Asn Tyr Gly Ser Phe Ala Glu
1 5 10

<210> 75
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 75
gca aga cat aac tac ggc agt ttt gct atg 30
Ala Arg His Asn Tyr Gly Ser Phe Ala Met
1 5 10

<210> 76
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 76
Ala Arg His Asn Tyr Gly Ser Phe Ala Met
1 5 10

<210> 77
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 77
gca aga cat aac tac ggc agt ttt gct ggg
Ala Arg His Asn Tyr Gly Ser Phe Ala Gly
1 5 10

30

<210> 78
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 78
Ala Arg His Asn Tyr Gly Ser Phe Ala Gly
1 5 10

<210> 79
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 79
gca aga cat aac tac ggc agt ttt gct gct
Ala Arg His Asn Tyr Gly Ser Phe Ala Ala
1 5 10

30

<210> 80
 <211> 10
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 80
 Ala Arg His Asn Tyr Gly Ser Phe Ala Ala
 1 5 10

<210> 81
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(39)

<220>
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 81
 cag gcc agc caa agt att agc aac ttt cta cac tgg tat 39
 Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr
 1 5 10

<210> 82
 <211> 13
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 82
 Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr
 1 5 10

<210> 83
 <211> 33

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(33)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 83
ctt ctc atc cgt tat tct tcc cag tcc atc tct
Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser
1 5 10

33

<210> 84
<211> 11
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 84
Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser
1 5 10

<210> 85
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(27)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 85
caa cag agt aat agc tgg cct cac acg
Gln Gln Ser Asn Ser Trp Pro His Thr
1 5

27

<210> 86
<211> 9
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 86
Gln Gln Ser Asn Ser Trp Pro His Thr
1 5

<210> 87
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(27)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 87
caa cag agt act agc tgg cct cac act
Gln Gln Ser Thr Ser Trp Pro His Thr
1 5

27

<210> 88
<211> 9
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 88
Gln Gln Ser Thr Ser Trp Pro His Thr
1 5

<210> 89
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(27)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 89
caa cag agt ggc agc tgg cct ctg acg
Gln Gln Ser Gly Ser Trp Pro Leu Thr
1 5

27

<210> 90
<211> 9
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 90
Gln Gln Ser Gly Ser Trp Pro Leu Thr
1 5

<210> 91
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(27)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 91
caa cag agt ggc agc tgg cct cag acg
Gln Gln Ser Gly Ser Trp Pro Gln Thr
1 5

27

<210> 92
 <211> 9
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 92
 Gln Gln Ser Gly Ser Trp Pro Gln Thr
 1 5

<210> 93
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(30)

<220>
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 93
 gca aga cat aac cat ggc agt ttt tat tct 30
 Ala Arg His Asn His Gly Ser Phe Tyr Ser
 1 5 10

<210> 94
 <211> 10
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Mutated
 complementarity determining region (CDR)

<400> 94
 Ala Arg His Asn His Gly Ser Phe Tyr Ser
 1 5 10

<210> 95
 <211> 30

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 95
gca aga cat aac cat ggc agt ttt gct tct
Ala Arg His Asn His Gly Ser Phe Ala Ser
1 5 10

30

<210> 96
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 96
Ala Arg His Asn His Gly Ser Phe Ala Ser
1 5 10

<210> 97
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 97
gca aga cat aac tac ggc agt ttt tat gag
Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu
1 5 10

30

<210> 98
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 98
Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu
1 5 10

<210> 99
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 99
gca aga cat aac tac ggc agt ttt tat tct 30
Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser
1 5 10

<210> 100
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 100
Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser
1 5 10

<210> 101
<211> 51

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(51)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 101
aaa gtt agt agt ggt ggt ggt agc acc tac tat tta gac act gtg cag 48
Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val Gln
1 5 10 15

ggc 51
Gly

<210> 102
<211> 17
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 102
Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val Gln
1 5 10 15

Gly

<210> 103
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(51)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 103

aaa gtt agt agt ggt ggt ggt agc acc tac tat cca gac act gtg cag 48
Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Thr Val Gln
1 5 10 15

ggc 51
Gly

<210> 104

<211> 17

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 104

Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Thr Val Gln
1 5 10 15

Gly

<210> 105

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(24)

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 105

cat ctt cat ggc agt ttt gct tct 24
His Leu His Gly Ser Phe Ala Ser
1 5

<210> 106

<211> 8

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 106

His Leu His Gly Ser Phe Ala Ser
1 5

<210> 107

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(33)

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 107

cag gcc agc caa agt att agc aac cac cta cac
Gln Ala Ser Gln Ser Ile Ser Asn His Leu His
1 5 10

33

<210> 108

<211> 11

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 108

Gln Ala Ser Gln Ser Ile Ser Asn His Leu His
1 5 10

<210> 109

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS
<222> (1)..(33)

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 109

cag gcc agc caa agt att agc aac ttc cta cac
Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His
1 5 10

33

<210> 110

<211> 11

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 110

Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His
1 5 10

<210> 111

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(21)

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 111

tat cgt tcc cag tcc atc tct
Tyr Arg Ser Gln Ser Ile Ser
1 5

21

<210> 112

<211> 7

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 112

Tyr Arg Ser Gln Ser Ile Ser

1

5